In the Claims:

1.   (Currently Amended) A method for analyzing data having a set of objects, the method comprising:

using a computer for performing ~~an unsupervised analysis of data according~~ at least one permutation of the objects to provide a reordered distance matrix describing distances between objects in the reordered set;

analyzing said reordered distance matrix so as to determine the structure of the data featured by said reordered distance matrix; and

displaying said structure of the data.

2.   (Original)   The method of claim 1, wherein said distance matrix is reordered using a weighting function.

3.   (Previously Presented)   The method of claim 1, suitable for automatically and semi-automatically analyzing data.

4.   (Previously Presented)   The method of claim 1, wherein the data comprises a plurality of objects characterized by continuous variables.

5.   (Previously Presented)   The method of claim 1, further comprising:

visualization of the data according to said analysis.

6.   (Original)   The method of claim 5, further comprising:

detecting at least one characteristic of the data according to said visualization.

7.   (Previously Presented)   The method of claim 1, further comprising:

detecting at least one characteristic of the data according to said analysis.

8. (Previously Presented) The method of claim 6, wherein the data is analyzed without reference to a predetermined order and/or wherein the data lacks pre-ordering.

9. (Canceled)

10. (Currently Amended) The method of claim ~~9~~1, wherein ~~the SPIN method~~ said performing said at least one permutation comprises the *Side-to-Side (STS)* method, featuring a strictly increasing or decreasing vector for reordering said distance matrix.

11. (Original) The method of claim 10, wherein said STS method comprises:

Input: D_{nxn} and a strictly increasing vector X

1. Compute $S = D\,X$.

2. Sort S in descending order to get $S' = P(S)$, where P is the sorting permutation.

3. If $P(S) \mathrel{!=} S$, set $D = P\,D\,P^{T}$ and go to *stage 1*.

4. Output D.

12. (Original) The method of claim 11, further comprising performing stages 1-3 more than once.

13. (Previously Presented) The method of claim 11, further comprising using at least one heuristic to reorder D.

14. (Currently Amended) The method of claim ~~9~~1, wherein ~~the SPIN method~~ said performing said at least one permutation comprises the *Neighborhood* method, featuring a matrix of fixed size.

15. (Original) The method of claim 14, wherein said Neighborhood method comprises:

Input : D_{nxn} and W_{nxn}

1. Compute $M = D\ W$

2. Set $P = \arg\min_{Q \in S_n} \operatorname{tr}(QM) \cdot$

3. If tr $(P\ M)$!= tr (M), set $D = P\ D\ PT$ and go to 1.

4. Output D.

16.   (Original)   The method of claim 15, further comprising performing stages 1-3 more than once.

17.   (Previously Presented)   The method of claim 15, further comprising using at least one heuristic to reorder D.

18.   (Original)   The method of claim 14, wherein the *Neighborhood* method features Gaussian smoothing.

19.   (Previously Presented)   The method of claim 15, wherein stage 2 is performed by solving the Linear Assignment Problem.

20.   (Previously Presented)   The method of claim 1, further comprising:

zooming in on a part of the data by separately examining a sub-matrix of the data according to said analysis.

21.   (Original)   The method of claim 20, further comprising:

separately examining a plurality of sub-matrices of the data according to said analysis; and

comparing results of said separate examinations to determine at least one characteristic of the data.

22.   (Previously Presented)   The method of claim 1, wherein the data comprises gene expression data and/or data from a gene microarray, comprising data from a large number of genes analyzed simultaneously.

23.   (Previously Presented)   The method of claim 1, wherein the data comprises data from expression of genes in cancerous tissue.

24.   (Withdrawn)   The method of claim 1, wherein the data comprises data related to a biological process, optionally including a biological cycle.

25.   (Withdrawn)   The method of claim 1 adapted for machine vision.

26.   (Currently Amended) A method for analyzing gene expression data and/or data from a gene microarray, comprising data from a large number of genes analyzed simultaneously, comprising:
        using a computer for filtering the data according to a variance filter to form filtered data; determining a distance matrix for said filtered data; and reordering performing at least one permutation of the objects in said distance matrix to provide a reordered distance matrix;
        analyzinge said filtered data reordered distance matrix so as to determine the structure of the data featured by said reordered distance matrix; and
        displaying said structure of the data.

27.   (Original)   The method of claim 26, further comprising:
        analyzing said reordered distance matrix to determine at least one characteristic of said filtered data.

28.   (Original)   The method of claim 27, wherein said reordering is performed according to an automatic and/or semi-automatic, unsupervised analysis.

29.   (Currently Amended) The method of claim 28, wherein said reordering is performed according to SPIN comprises performing at least one permutation of said objects.

30.   (Previously Presented)   The method of claim 27, wherein the data is analyzed to determine a noise level in the data.

31.   (Original)   The method of claim 30, wherein said noise level is used to alter at least one characteristic of the microarray or of an experimental protocol for data collection.

32.   (Previously Presented)   The method of claim 27, wherein the data is analyzed to determine an inherent property of the data other than a property for which the experiment was designed.

33.   (Previously Presented)   The method of claim 26, wherein the data comprises cancer-related data.

34.   (Original)   The method of claim 26, adapted for ordering both samples and genes.

35.   (Withdrawn and Currently Amended)   A—The method of claim 1 wherein the for analyzing data related to a biological process, optionally including a biological cycle, comprising the SPIN method.

36.   (Withdrawn and Currently Amended)   A—The method of claim 1 wherein the data comprises visual data and the method is employed for machine vision, comprising the SPIN method.

37.   (Canceled)

38.   (Withdrawn and Currently Amended)   The method of claim 3736, further comprising:
        zooming in on a part of the data by separately examining a sub-matrix of the data according to said analysis.

39.   (Withdrawn)   The method of claim 38, further comprising:
        separately examining a plurality of sub-matrices of the data according to said analysis; and

comparing results of said separate examinations to determine at least one characteristic of the data.

40.   (Currently Amended) A method according to claim 1, for partitioning the data into a plurality of ~~optionally overlapping~~ subsets.

41.   (Original)   The method of claim 40, further comprising:

using the distance matrices calculated from each subset separately to find novel partitions.

42.   (Canceled)

43.   (Currently Amended) ~~A~~ The method of claim 1, wherein the ~~for analyzing~~ data relate to ~~from~~ expression of genes in cancerous tissue~~, comprising the SPIN method~~.

44.   (Previously Presented)   The method of claim 1, further comprising optionally constraining said reordering according to a dendrogram from any hierarchical clustering method.

45.   (New) The method of claim 40, wherein said plurality of subsets comprises a plurality of overlapping subsets.

46.   (New) The method of claim 1, wherein said performing said at least one permutation of the objects to provide said reordered distance matrix comprises searching for a minimum of an energy function.

47.   (New) The method of claim 26, wherein said performing said at least one permutation of the objects to provide said reordered distance matrix comprises searching for a minimum of an energy function.